

## APPENDIX

## Changes to Claims:

The following are marked-up versions of the amended claims:

1. (Amended) Nucleic material, in isolated or purified state, comprising a nucleotide sequence chosen from the group which consists of (i) the sequences SEQ ID NO: ~~4124~~, SEQ ID NO: ~~4146~~, SEQ ID NO: ~~4179~~, SEQ ID NO: 120, SEQ ID NO: ~~42416~~, SEQ ID NO: ~~43021~~, SEQ ID NO: ~~44130~~ and SEQ ID NO: ~~44231~~; (ii) the sequences complementary to sequences (i); and (iii) the sequences equivalent to sequences (i) or (ii), in particular the sequences having, for every series of 100 contiguous monomers, at least 50%, and preferentially at least 70% homology with sequences (i) or (ii) respectively.
2. (Amended) Nucleic material, in isolated or purified state, encoding a polypeptide having, for every contiguous series of at least 30 amino acids, at least 50%, and preferably at least 70% homology with a peptide sequence chosen from the group which consists of SEQ ID NO: ~~4135~~, SEQ ID NO: ~~4157~~, SEQ ID NO: ~~41810~~, SEQ ID NO: ~~42413~~, SEQ ID NO: ~~43525~~ and SEQ ID NO: ~~43726~~.
3. (Amended) Retroviral nucleic material, whose pol gene comprises a nucleotide sequence identical or equivalent to a sequence chosen from the group which consists of SEQ ID NO: ~~4124~~, SEQ ID NO: ~~42416~~ and their complementary sequences.
4. (Amended) Retroviral nucleic material, in which the 5' end of the pol gene starts at nucleotide 1419 of SEQ ID NO: ~~43021~~.
5. (Amended) Retroviral nucleic material, in which the pol gene encodes a polypeptide having, for every contiguous series of at least 30 amino acids, at least 50%, and preferably at least 70% homology with the peptide sequence SEQ ID NO: ~~4135~~.
6. (Amended) Retroviral nucleic material, in which the 3' end of the gag gene ends at nucleotide 1418 of SEQ ID NO: ~~43021~~.

7. (Amended) Retroviral nucleic material, in which the env gene comprises a nucleotide sequence identical or equivalent to a sequence chosen from the group which consists of SEQ ID NO: 4479, and its complementary sequences.
8. (Twice Amended) Retroviral nucleic material, in which the env gene comprises a nucleotide sequence which starts at nucleotide 1 of SEQ ID NO: 4479 and ends at nucleotide 233 of SEQ ID NO: 4446.
9. (Amended) Retroviral nucleic material, in which the env gene encodes a polypeptide having, for every contiguous series of at least 30 amino acids, at least 50%, and preferably at least 70% homology with the sequence SEQ ID NO: 44810.
10. (Amended) Retroviral nucleic material in which the U3R region of the 3' LTR comprises a nucleotide sequence which ends at nucleotide 617 of SEQ ID NO: 4446.
11. (Amended) Retroviral nucleic material in which the RU5 region of the 5' LTR comprises a nucleotide sequence which starts at nucleotide 755 of SEQ ID NO: 120 and ends at nucleotide 337 of SEQ ID NO: 44130 or SEQ ID NO: 44231.
12. (Amended) Retroviral nucleic material comprising a sequence which starts at nucleotide 755 of SEQ ID NO: 120 and which ends at nucleotide 617 of SEQ ID NO: 4446.
14. (Amended) Nucleotide fragment comprising a nucleotide sequence chosen from the group which consists of (i) the sequences SEQ ID NO: 4424, SEQ ID NO: 4446, SEQ ID NO: 4479, SEQ ID NO: 120, SEQ ID NO: 42416, SEQ ID NO: 43021, SEQ ID NO: 44130 and SEQ ID NO: 44231; (ii) the sequences complementary to sequences (i); and (iii) the sequences equivalent to sequences (i) or (ii), in particular the sequences having, for every series of 100 contiguous monomers, at least 50%, and preferentially at least 70% homology with sequences (i) or (ii) respectively.
15. (Amended) Nucleotide fragment according to Claim 14, consisting of a nucleotide sequence chosen from the group which consists of (i) the sequences SEQ ID

NO: 4124, SEQ ID NO: 4146, SEQ ID NO: 4179, SEQ ID NO: 129, SEQ ID NO: 42416, SEQ ID NO: 43021, SEQ ID NO: 44130 and SEQ ID NO: 44231; (ii) the sequences complementary to sequences (i); and (iii) the sequences equivalent to sequences (i) or (ii), in particular the sequences having, for every series of 100 contiguous monomers, at least 50%, and preferentially at least 70% homology with sequences (i) or (ii) respectively.

16. (Amended) Nucleotide fragment comprising a nucleotide sequence encoding a polypeptide having, for every contiguous series of at least 30 amino acids, at least 50%, and preferably at least 70% homology with a peptide sequence chosen from the group which consists of SEQ ID NO: 4135, SEQ ID NO: 4157, SEQ ID NO: 41810, SEQ ID NO: 42413, SEQ ID NO: 43525 and SEQ ID NO: 43726.

17. (Amended) Nucleotide fragment according to claim 16, consisting of a nucleotide sequence encoding a polypeptide having, for every contiguous series of at least 30 amino acids, at least 50%, and preferably at least 70% homology with a peptide sequence chosen from the group which consists of SEQ ID NO: 4135, SEQ ID NO: 4157, SEQ ID NO: 41810, SEQ ID NO: 42413, SEQ ID NO: 43525 and SEQ ID NO: 43726.

21. (Amended) Primer according to claim 20, characterized in that its nucleotide sequence is chosen from SEQ ID NO: 4168, SEQ ID NO: 119, SEQ ID NO: 42214, SEQ ID NO: 42315, SEQ ID NO: 42617, SEQ ID NO: 42718, SEQ ID NO: 42819, SEQ ID NO: 42920, SEQ ID NO: 43223, and SEQ ID NO: 43324.

24. (Amended) Peptide according to claim 23 comprising a sequence identical, partially or completely, or equivalent to a sequence chosen from SEQ ID NO: 4135, SEQ ID NO: 4157, SEQ ID NO: 41810, SEQ ID NO: 42413, SEQ ID NO: 43525 and SEQ ID NO: 43726.